STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _/0/537,839_

Source: _PCT/10_

Date Processed by STIC: _6/16/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> **http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission **User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 10/537,839

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics / Wrapped Aminos   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES)   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/537,839

DATE: 06/16/2005
TIME: 10:18:53

Input Set : A:\pto.da.txt
Output ·Set: N:\CRF4\06162005\J537839.raw

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IN
   4       QUEENSLAND
   6 <120> TITLE OF INVENTION: NOVEL THERAPEUTIC MOLECULES AND USES THEREOF
   8 <130> FILE REFERENCE: 12381870/TDO
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C--> 10 <141> CURRENT FILING DATE: 2005-06-06
  10 <150> PRIOR APPLICATION NUMBER: 2002953223
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  13 <160> NUMBER OF SEQ ID NOS: 32
  15 <170> SOFTWARE: PatentIn version 3.1
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pp 12-13

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

P. 12

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RAW SEQUENCE LISTING   DATE: 06/16/2005
PATENT APPLICATION: US/10/537,839   TIME: 10:18:53

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\06162005\J537839.raw

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4204 gtctgaaaaa tagagcagtc agggaagcca agtgagtagg agataacttc aaggctggac 25140
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4208 ataaagagat cattggtgac ctctgccaca gaaatttctg aagaaatgtt gagaaaatgg 25260
4210 attaaatggg cttaagaaat gaaaaagtga gcttgtttca gtgtttgctg tttcctcaag 25320
4212 taaggaacat tgttaggcta aaaagtattt ttcctaaatt ttgtttcttt aaaaaaaaca 25380
4214 ggatttcatg gtaaatagct attatatgct gtcaagcaag caatggacct ttcctttaat 25440
4216 taatgaggta gataatacat ttcctaatgt aaaactatcc taacctccag atataaacta 25500
4218 cacattgttt taatacactg cttatcagtt gccttgacaa ttgactttgt cacacatttt 25560
4220 agtagtatgc agctagctaa ctaaaacccc tggaggcaac tttggctaaa ggtcacttgc 25620
4222 agaatgtgaa aagcagcata tatacttact gtgtctcgcc catcttggac actgtccagt 25680
4224 tcttaggata cccggtcttt taaagctatt atgattgagt ctgtaaatat ttctcaatta 25740
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RAW SEQUENCE LISTING   DATE: 06/16/2005
PATENT APPLICATION: US/10/537,839   TIME: 10:18:53

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\06162005\J537839.raw

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E--> 4457 - 3 -

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<210>   23
<211>   21
<212>   DNA
<213>   (synthetic)

<400>   23
gaccatggag cggacatgat a                                          21
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invalid <213> response

see item 10 on

Error Summary

Sheet

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY   DATE: 06/16/2005
PATENT APPLICATION: **US/10/537,839**   TIME: 10:18:54

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\06162005\J537839.raw**

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:25
L:1231 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:1229
L:1609 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:1606
L:1810 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:1807
L:1812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:48
M:341 Repeated in SeqNo=10
L:1901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:2010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:2040 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:2037
L:2069 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:2067
L:2096 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:2094
L:2125 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:2123
L:4457 M:254 E: No. of Bases conflict, this line has no nucleotides.
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